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<110> Lechler, Robert I.  
Dorling, Anthony

<120> IMMUNOSUPPRESSION BY BLOCKING T CELL CO-STIMULATION SIGNAL 2 (B7/CD28 INTERACTION)

<130> 2292/0H795

<140> US 09/674,462

<141> 2001-05-08

<150> PCT/ GB99/01350

<151> 1999-04-30

<160> 27

<170> PatentIn Ver. 2.1

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<211> 223

<212> PRT

<213> Sus scrofa

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Val Phe Ser Lys Gly Met His Val Ala Gln Pro Ala Val Val Leu Ala  
35 40 45

Asn Ser Arg Gly Val Ala Ser Phe Val Cys Glu Tyr Gly Ser Ala Gly  
50 55 60

Lys Ala Ala Glu Val Arg Val Thr Val Leu Arg Arg Ala Gly Ser Gln  
65 70 75 80

Met Thr Glu Val Cys Ala Ala Thr Tyr Thr Val Glu Asp Glu Leu Thr  
85 90 95

Phe Leu Asp Asp Ser Thr Cys Thr Gly Thr Ser Thr Glu Asn Lys Val  
100 105 110

Asn Leu Thr Ile Gln Gly Leu Arg Ala Val Asp Thr Gly Leu Tyr Ile  
115 120 125

Cys Lys Val Glu Leu Leu Tyr Pro Pro Pro Tyr Tyr Val Gly Met Gly  
 130 135 140

Asn Gly Thr Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser  
 145 150 155 160

Asp Phe Leu Leu Trp Ile Leu Ala Ala Val Ser Ser Gly Leu Phe Phe  
 165 170 175

Tyr Ser Phe Leu Ile Thr Ala Val Ser Leu Ser Lys Met Leu Lys Lys  
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Arg Ser Pro Leu Thr Thr Gly Val Tyr Val Lys Met Pro Pro Thr Glu  
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 gcccaacctg cagtagtgct ggccaacagc cggggtgttg ccagctttgt gtgtgagtat 180  
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Asn	Ser	Arg	Gly	Val	Ala	Ser	Phe	Val	Cys	Glu	Tyr	Gly	Ser	Ala	Gly
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Lys	Ala	Ala	Glu	Val	Arg	Val	Thr	Val	Leu	Arg	Arg	Ala	Gly	Ser	Gln
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Met	Thr	Glu	Val	Cys	Ala	Ala	Thr	Tyr	Thr	Val	Glu	Asp	Glu	Leu	Thr
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Phe	Leu	Asp	Asp	Ser	Thr	Cys	Thr	Gly	Thr	Ser	Thr	Glu	Asn	Lys	Val
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Cys	Lys	Val	Glu	Leu	Leu	Tyr	Pro	Pro	Pro	Tyr	Tyr	Val	Gly	Met	Gly
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Asp	Gly	Gly	Ser	Gly	Gly	Ala	Ala	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr
				165					170					175	
His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser
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Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu  
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 Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys  
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 Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser  
 325 330 335  
 Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp  
 340 345 350  
 Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser  
 355 360 365  
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<210> 5  
 <211> 240  
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Ala	Met	Ser 35	Trp	Val	Arg	Gln	Ala 40	Pro	Gly	Lys	Gly	Leu 45	Glu	Trp	Val
Ser	Ala 50	Ile	Ser	Gly	Ser	Gly 55	Gly	Ser	Thr	Tyr	Tyr 60	Ala	Asp	Ser	Val
Lys 65	Gly	Arg	Phe	Thr	Ile 70	Ser	Arg	Asp	Asn	Ser 75	Lys	Asn	Thr	Leu	Tyr 80
Leu	Gln	Met	Asn	Ser 85	Leu	Arg	Ala	Glu	Asp 90	Thr	Ala	Val	Tyr	Tyr 95	Cys
Ala	Arg	Ala	Gly 100	Arg	Ile	Leu	Phe	Asp 105	Tyr	Trp	Gly	Gln	Gly 110	Thr	Leu
Val	Thr 115	Val	Ser	Ser	Gly	Gly	Gly 120	Gly	Ser	Gly	Gly	Gly 125	Gly	Ser	Gly
Gly 130	Ser	Ala	Leu	Gln	Ser	Val 135	Leu	Thr	Gln	Pro	Pro 140	Ser	Ala	Ser	Gly
Thr 145	Pro	Gly	Gln	Arg	Val 150	Thr	Ile	Ser	Cys	Ser 155	Gly	Ser	Ser	Ser	Asn 160
Ile	Gly	Ser	Asn	Tyr 165	Val	Tyr	Trp	Tyr	Gln 170	Gln	Leu	Pro	Gly	Thr 175	Ala
Pro	Lys	Leu	Leu 180	Ile	Tyr	Arg	Asn	Asn 185	Gln	Arg	Pro	Ser	Gly 190	Val	Pro
Asp	Arg	Phe 195	Ser	Gly	Ser	Lys	Ser 200	Gly	Thr	Ser	Ala	Ser 205	Leu	Ala	Ile
Ser	Gly 210	Leu	Arg	Ser	Glu	Asp 215	Glu	Ala	Asp	Tyr	Tyr 220	Cys	Ala	Ala	Trp
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<213> Phage library
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gccagatgcc	cgggaaaggc	ctggagtgga	tggggatcat	ctatcctggg	gactctgata	180
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cctggtctat	gctgcatcca	ctttgcaaag	tgggggccca	tcaagggtca	gcggcagtg	600
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<210> 10
<211> 240
<212> PRT
<213> Phage library
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Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
          35             40             45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
          50             55             60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

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65					70						75				80
Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
				85					90					95	
Ala	Arg	Ala	Gly	Arg	Ile	Leu	Phe	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Leu
			100					105					110		
Val	Thr	Val	Ser	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly
		115					120					125			
Gly	Ser	Ala	Leu	Gln	Ser	Val	Leu	Thr	Gln	Pro	Pro	Ser	Ala	Ser	Gly
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Thr	Pro	Gly	Gln	Arg	Val	Thr	Ile	Ser	Cys	Ser	Gly	Ser	Ser	Ser	Asn
145					150					155					160
Ile	Gly	Ser	Asn	Tyr	Val	Tyr	Trp	Tyr	Gln	Gln	Leu	Pro	Gly	Thr	Ala
				165					170					175	
Pro	Lys	Leu	Leu	Ile	Tyr	Arg	Asn	Asn	Gln	Arg	Pro	Ser	Gly	Val	Pro
			180					185					190		
Asp	Arg	Phe	Ser	Gly	Ser	Lys	Ser	Gly	Thr	Ser	Ala	Ser	Leu	Ala	Ile
		195					200					205			
Ser	Gly	Leu	Arg	Ser	Glu	Asp	Glu	Ala	Ser	Tyr	Tyr	Cys	Ala	Ala	Trp
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 <211> 246  
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 35 40 45



Leu Glu Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Asn Tyr Asn  
 50 55 60  
 Pro Ser Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn  
 65 70 75 80  
 Gln Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val  
 85 90 95  
 Tyr Tyr Cys Ala Arg Met Arg Lys Asp Lys Phe Asp Tyr Trp Gly Gln  
 100 105 110  
 Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly  
 115 120 125  
 Gly Ser Gly Gly Ser Ala Leu Gln Ser Val Leu Thr Gln Pro Pro Ser  
 130 135 140  
 Ala Ser Gly Thr Pro Gly Gln Arg Val Thr Ile Ser Cys Ser Gly Ser  
 145 150 155 160  
 Ser Ser Asn Ile Gly Ser Asn Tyr Val Tyr Trp Tyr Gln Gln Leu Pro  
 165 170 175  
 Gly Thr Ala Pro Lys Leu Leu Ile Tyr Arg Asn Asn Gln Arg Pro Ser  
 180 185 190  
 Gly Val Pro Asp Arg Phe Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser  
 195 200 205  
 Leu Ala Ile Ser Gly Leu Arg Ser Glu Asp Glu Ala Asp Tyr Tyr Val  
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<211> 242

<212> PRT

<213> Phage library

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 35 40 45  
 Gly Ile Ile Asn Pro Ser Gly Gly Ser Thr Ser Tyr Ala Gln Lys Phe  
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 Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr  
 65 70 75 80  
 Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys  
 85 90 95  
 Ala Arg Val Ala Pro Tyr Val Asn Thr Leu Val Phe Trp Gly Gln Gly  
 100 105 110  
 Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly  
 115 120 125  
 Ser Gly Gly Ser Ala Leu Ser Ser Glu Leu Thr Gln Asp Pro Ala Val  
 130 135 140  
 Ser Val Ala Leu Gly Gln Thr Val Arg Ile Thr Cys Gln Gly Asp Ser  
 145 150 155 160  
 Leu Arg Ser Tyr Tyr Ala Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ala  
 165 170 175  
 Pro Val Leu Val Ile Tyr Gly Lys Asn Asn Arg Pro Ser Gly Ile Pro  
 180 185 190  
 Asp Arg Phe Ser Gly Ser Ser Ser Gly Asn Thr Ala Ser Leu Thr Ile  
 195 200 205  
 Thr Gly Ala Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Asn Ser Arg  
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Leu Gly

<210> 13

<211> 240

<212> PRT

<213> Phage library

<400> 13

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Trp	Ile	Gly 35	Trp	Val	Arg	Gln	Met 40	Pro	Gly	Lys	Gly	Leu 45	Glu	Trp	Met
Gly	Ile 50	Ile	Tyr	Pro	Gly	Asp 55	Ser	Asp	Thr	Arg	Tyr 60	Ser	Pro	Ser	Phe
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Val	Thr 115	Val	Ser	Ser	Gly	Gly	Gly 120	Gly	Ser	Gly	Gly	Gly 125	Gly	Ser	Gly
Gly 130	Ser	Ala	Leu	Asp	Ile	Gln 135	Leu	Thr	Gln	Ser	Pro 140	Ser	Phe	Leu	Ser
Ala 145	Ser	Val	Gly	Asp	Arg 150	Val	Thr	Ile	Thr	Cys 155	Arg	Ala	Ser	Gln	Gly 160
Ile	Ser	Ser	Tyr	Leu 165	Ala	Trp	Tyr	Gln	Gln 170	Lys	Pro	Gly	Lys	Ala 175	Pro
Lys	Leu	Leu	Val 180	Tyr	Ala	Ala	Ser	Thr 185	Leu	Gln	Ser	Gly	Val 190	Pro	Ser
Arg	Phe	Ser 195	Gly	Ser	Gly	Ser	Gly 200	Thr	Glu	Phe	Thr	Leu 205	Thr	Ile	Ser
Ser 210	Leu	Gln	Pro	Glu	Asp	Phe 215	Ala	Thr	Tyr	Tyr	Cys 220	Gln	Gln	Leu	Asn
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<210> 14  
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 <212> DNA  
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 ttctcctcac agctgtttct ttgagcaaaa tgctaaagaa aagaagccct cttacaacag 660  
 gggctctatgt gaaaatgccc ccaacagagc cagaatgtga aaagcaattt cagccttatt 720  
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 <213> Homo sapiens

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 Thr Arg Thr Trp Pro Cys Thr Leu Leu Phe Phe Leu Leu Phe Ile Pro  
                   20                  25                  30  
 Val Phe Cys Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala  
                   35                  40                  45  
 Ser Ser Arg Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Gly  
   50                  55                  60  
 Lys Ala Thr Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln  
   65                  70                  75                  80  
 Val Thr Glu Val Cys Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr  
                   85                  90                  95  
 Phe Leu Asp Asp Ser Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val  
                   100                  105                  110  
 Asn Leu Thr Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile  
                   115                  120                  125

Cys Lys Val Glu Leu Met Tyr Pro Pro Pro Tyr Tyr Leu Gly Ile Gly  
 130 135 140  
 Asn Gly Thr Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser  
 145 150 155 160  
 Asp Phe Leu Leu Trp Ile Leu Ala Ala Val Ser Ser Gly Leu Phe Phe  
 165 170 175  
 Tyr Ser Phe Leu Leu Thr Ala Val Ser Leu Ser Lys Met Leu Lys Lys  
 180 185 190  
 Arg Ser Pro Leu Thr Thr Gly Val Tyr Val Lys Met Pro Pro Thr Glu  
 195 200 205  
 Pro Glu Cys Glu Lys Gln Phe Gln Pro Tyr Phe Ile Pro Ile Asn  
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 aaccgcagct cgggctgctc gtggctcttc cagccgcgcg gcgccgccgc cagtcccacc 240  
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 aacgagggct actatttctg ctcggccctg agcaactcca tcatgtactt cagccacttc 420  
 gtgccggtct tcttgccagc gaagcccacc acgacgccag cgccgcgacc accaacaccg 480  
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 gggggcgag tgcacacgag ggggctggac ttgcgctgtg atatctacat ctgggcgccc 600  
 ttggccggga cttgtggggg ccttctcctg tcaactgtta tcacccttta ctgcaaccac 660  
 aggaaccgaa gacgtgtttg caaatgtccc cggcctgtgg tcaaactcggg agacaagccc 720  
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33

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25

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22

<210> 22  
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33

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29

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33

<210> 27

<211> 73

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<213> Artificial Sequence

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<223> PCR primer

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tgatatctac atc

73